

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;  
CO, Man S.

(ii) TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF  
MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR  
PREVENTION OF ACUTE ORGAN DAMAGE AFTER  
EXTRACORPOREAL BLOOD CIRCULATION

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Felfe & Lynch  
(B) STREET: 805 Third Avenue  
(C) CITY: New York  
(D) STATE: New York  
(E) COUNTRY: U.S.A.  
(F) ZIP: 10022

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Computer Disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: ASCII, WordPerfect 5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/578,953  
(B) FILING DATE: 27-Dec-95  
(C) CLASSIFICATION: 530

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP 95 112 895.8  
(B) FILING DATE: 17-Aug-95  
(A) APPLICATION NUMBER: EP 95 114 969.9  
(B) FILING DATE: 19-Sep-95

(viii) ATTORNEY/AGENT INFORMATION

(A) NAME: Hanson, Norman D.  
(B) REGISTRATION NUMBER: 30,946  
(C) REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH

(ix) TELECOMMUNICATION INFORMATION

(A) TELEPHONE: (212) 688-9200  
(B) TELEFAX: (212) 838-3884

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1,,654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAC ATT CAG ATG ACC CAA TCT CCG AGC TCT TTG TCT GCG TCT GTA GGG	48
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly	
1 5 10 15	
GAT AGG GTC ACT ATC ACC TGC AAG GCC AGC CAA AGT GTT GAT TAT GAT	96
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp	
20 25 30	
GGT GAT AGT TAT ATG AAC TGG TAC CAA CAG AAA CCA GGA AAG GCA CCC	144
Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro	
35 40 45	
AAG CTT CTC ATC TAT GCT GCA TCC AAC CTA GAA TCT GGT ATC CCA TCC	192
Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ser	
50 55 60	
AGG TTT AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC CTC ACC ATC TCT	240
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser	
65 70 75 80	
TCT CTG CAG CCG GAG GAT TTC GCA ACC TAT TAC TGT CAG CAA AGT AAT	288
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn	
85 90 95	
GAA GAT CCG TGG ACG TTC GGT CAA GGC ACC AAG GTG GAA ATC AAA CGA	336
Glu Asp Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg	
100 105 110	
ACT GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG CAG	384
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln	
115 120 125	
TTG AAA TCT GGA ACT GCC TCT GTT GTG TGC CTG CTG AAT AAC TTC TAT	432
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr	
130 135 140	

Biological Sciences

CCC	AGA	GAG	GCC	AAA	GTA	CAG	TGG	AAG	GTG	GAT	AAC	GCC	CTC	CAA	TCG	480
Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	
145					150				155					160		
GGT	AAC	TCC	CAG	GAG	AGT	GTC	ACA	GAG	CAG	GAC	AGC	AAG	GAC	AGC	ACC	528
Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	
			165					170					175			
TAC	AGC	CTC	AGC	AGC	ACC	CTG	ACG	CTG	AGC	AAA	GCA	GAC	TAC	GAG	AAA	576
Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	
			180					185					190			
CAC	AAA	GTC	TAC	GCC	TGC	GAA	GTC	ACC	CAT	CAG	GGC	CTG	AGC	TCG	CCC	624
His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	
		195					200					205				
GTC	ACA	AAG	AGC	TTC	AAC	AGG	GGA	GAG	TGT							654
Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys							
	210					215										

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5				10					15			
Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Ser	Val	Asp	Tyr	Asp	
		20					25					30				
Gly	Asp	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	
		35				40					45					
Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Ile	Pro	Ser	
	50				55					60						
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	
65				70				75						80		
Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Asn	
			85					90						95		
Glu	Asp	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	
		100				105						110				

Sequence = T A C C A A G

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln  
 115 120 125  
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr  
 130 135 140  
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser  
 145 150 155 160  
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
 165 170 175  
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
 180 185 190  
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro  
 195 200 205  
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 210 215

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1329 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1,,1329

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION:1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GAA GTG CAA CTG GTG GAG TCT GGG GGA GGC TTA GTG CAG CCT GGA GGA 48  
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 AGC TTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACT TTC AGT ACC TAT 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr  
 20 25 30  
 GCC ATG TCT TGG GTT CGC CAG GCT CCA GGG AAG GGA CTC GAG TGG GTC 144  
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

GCA	TCC	ATT	AGT	ACT	GGT	GGT	AGC	ACC	TAC	TAT	CCA	GAC	AGT	GTG	AAG	192
Ala	Ser	Ile	Ser	Thr	Gly	Gly	Ser	Thr	Tyr	Tyr	Pro	Asp	Ser	Val	Lys	
	50					55					60					
GGC	CGA	TTC	ACC	ATC	TCC	AGA	GAT	AAT	GCC	AAG	AAC	ACC	CTG	TAC	CTG	240
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	
	65				70				75						80	
CAA	ATG	AAT	TCT	CTG	AGG	GCT	GAG	GAC	ACG	GCC	GTG	TAT	TAC	TGT	GCA	288
Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
			85						90					95		
AGA	GAC	TAT	GAC	GGG	TAT	TTT	GAC	TAC	TGG	GGC	CAA	GGC	ACC	CTG	GTC	336
Arg	Asp	Tyr	Asp	Gly	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	
			100					105						110		
ACA	GTC	TCC	TCA	GCT	TCC	ACC	AAG	GGC	CCA	TCC	GTC	TTC	CCC	CTG	GCG	384
Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	
			115				120						125			
CCC	TGC	TCC	AGG	AGC	ACC	TCC	GAG	AGC	ACA	GCC	GCC	CTG	GGC	TGC	CTG	432
Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	
	130					135					140					
GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA	GGC	480
Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	
	145				150					155					160	
GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	528
Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	
				165					170					175		
GGA	CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	576
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	
			180					185					190			
GGC	ACG	AAG	ACC	TAC	ACC	TGC	AAC	GTA	GAT	CAC	AAG	CCC	AGC	AAC	ACC	624
Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	
		195					200					205				
AAG	GTG	GAC	AAG	AGA	GTT	GAG	TCC	AAA	TAT	GGT	CCC	CCA	TGC	CCA	TCA	672
Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Ser	
	210					215					220					
TGC	CCA	GCA	CCT	GAG	TTC	CTG	GGG	GGA	CCA	TCA	GTC	TTC	CTG	TTC	CCC	720
Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	
	225				230					235					240	
CCA	AAA	CCC	AAG	GAC	ACT	CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACG	768
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	
				245					250					255		

TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAG	GAA	GAC	CCC	GAG	GTC	CAG	TTC	AAC	816
Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	
			260					265					270			
TGG	TAC	GTG	GAT	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	CGG	864
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	
		275					280					285				
GAG	GAG	CAG	TTC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC	CTC	ACC	GTC	912
Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	
	290					295					300					
CTG	CAC	CAG	GAC	TGG	CTG	AAC	GGC	AAG	GAG	TAC	AAG	TGC	AAG	GTC	TCC	960
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	
305					310					315					320	
AAC	AAA	GGC	CTC	CCG	TCC	TCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA	1008
Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	
			325						330					335		
GGG	CAG	CCC	CGA	GAG	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CAG	GAG	1056
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	
			340					345					350			
GAG	ATG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	1104
Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	
		355					360					365				
TAC	CCC	AGC	GAC	ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	1152
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	
	370					375					380					
AAC	AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	1200
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	
385					390					395					400	
TTC	CTC	TAC	AGC	AGG	CTA	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	GAG	GGG	1248
Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	
			405					410					415			
AAT	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	TAC	1296
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	
			420				425					430				
ACA	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CTG	GGT	AAA						1329
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys						
		435				440										

Sequence 1

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443
- (B) TYPE: amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr  
20 25 30  
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ala Ser Ile Ser Thr Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys  
50 55 60  
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu  
65 70 75 80  
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95  
Arg Asp Tyr Asp Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110  
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala  
115 120 125  
Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu  
130 135 140  
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly  
145 150 155 160  
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser  
165 170 175  
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu  
180 185 190  
Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr  
195 200 205  
Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser  
210 215 220

Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro  
 225 230 235 240  
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr  
 245 250 255  
 Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn  
 260 265 270  
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg  
 275 280 285  
 Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val  
 290 295 300  
 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser  
 305 310 315 320  
 Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys  
 325 330 335  
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu  
 340 345 350  
 Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe  
 355 360 365  
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu  
 370 375 380  
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe  
 385 390 395 400  
 Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly  
 405 410 415  
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr  
 420 425 430  
 Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys  
 435 440

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:







